

FIGURE 1

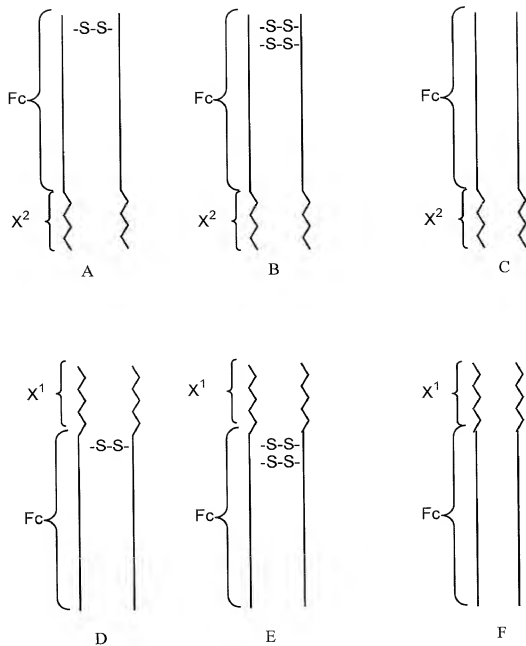
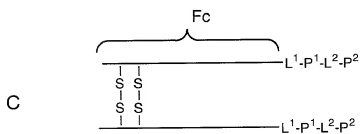
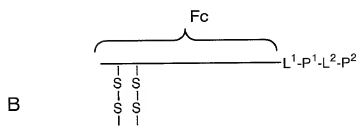
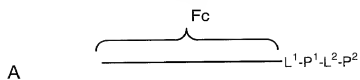


FIGURE 2



ATGGACAAAACTCACACATGTCCACCTTGTCAGCTCCGGAACCTCCTGGGGGGACCGTCA

1
TACC TGT TTT GAG AGT GTG TCA CAG GTT GGA AAC AGG TCG AGG CCT TGA GGA CCCCC TGG CAG T 60
a M D K T H T C T C P P C A P A P E L L G G P S -
61
GTC TCT C TCT TCCCC CCAA AAC CAA GAG CAC CCCC TCA TGA TCT CCG GAC CCCC TAG GTG C 120
a CAGA AGG AGA GAG GGG GGG TTT TGG GTT CTCT GGG AGT ACTAG AGG CCTGG GAC TCCAG
121
V F L F P P P K P K D T L L M I S R T P E V -
121
ACT TCG CTGT GGT GAG CACT GAG CCA GAG CAG CTGAG GTCA AGT TCA AGT TCG TGA CCG T 180
a TGT AGC CAC CAC CAC CTG CACT CGG TGT CTT C GGA CTT CCA GTT CAA GTT GAC CATG CAC
181
T C V V V D V S H E D P E V K F N W Y V -
181
GAC GCG CTGG AGG TGC ATA TGT CCA AGCAA AGC CGCG GAG GAG CAG TACA AAC CAG CAC G 240
a CTGG CGC ACC TCC CAG TAT TAC GTT C TGT TCG GCG CCCC TCT CGT CAT GTT GTT CGT GC
241
D G V E V H N A K T K P R E E Q Y N S T -
241
TAC CGT GTGT CAG CCG TCT CAC CCG TCT CAC CAG CAG TGG CTTGA ATG CCA AGG AGTAC 300
a ATG GCAC CAC CAG TCG CAG AGT GGC AGC GTG CTTGAC GACTTAC CGT TCC TCA TGT
301
Y R V V S V L T V L H Q D W L N G K E Y -
301
AAG TGA CAG GTCTCCA CCAA GCG CTTCC AGC CCCC ATCGA GAA AAC CATCTCCA AAG CC 360
a TTC ACG TCC CAG AGT TGT TTT CGG GAG GGT CGG GGT AGC TTT TGG TAG AGG TTT CGG
361
K C K V S N K A L P A P I E K T I S K A -
361
AAAG GCG AGC CCG GAG AAC CAC AGG TGTAC ACC CTTGCC CCCC ATCCG GAG TGA CCG TGA CC 420
a TTT CCG CTG CCG GGT CTTGG TGTCC CACTGTGG GAG CCGGG GTAGG GCC TACT CCA GTG
421
K Q G P R E P Q V Y T L P P S R D E L T -
421
AAGA ACC AGGT CAG CCTG ACC TGC CTTG TCAA AGG CTTCTAT CCCC AGC ATATCG CCG GTG 480
a TTT CTTG TCC AGT CCG CACTGG ACG CAC CAG TTTCCA AGATAGG GTCGT CTTAG CCG CAC
481
K N Q V S L T C L V K G F Y P S D I A V -
481
GAG TGG GAG AGC AATGG GCAG CCG GAG AACCA ACTACA AGC ACC CCG CTTCC GTT GGTGAC 540
a CTCA CCG CTTCTG TTA CCG CTG CCG CTTGTG TATG TCTGT GGTGG GAG GGC CAG CAC CTG
541
E W E S N C G Q P E N N Y K T T T P P V L D -
541
TCC GAC CGG CTCTCTCT CTTCTAC AGCA AGCTCAC CCG TGG ACA AGC CAG GTG CAG CAG 600
a AGG CTGCC GAG GAAAG GAG ATG TCG TCC AGTGG CAC CTG TCTCG TCC CAC CCG TCG TC
601
S D G S F F L Y S K L T V D K S R W Q Q -
601
GGGA ACG TCTTCTCAT GCTCC GTATG CATGAG GCG CTTG CACA ACC CACTTAC CCG CAG AG 660
a CCC TTC GCA AGAG GTAC GAG CAC TAC CTTCC GAG CAG CTG TGTG TATG TCG TCTCTC

FIGURE 3B

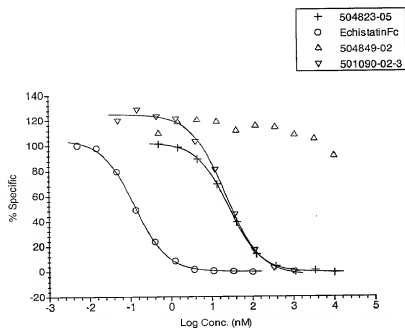
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      AGCCTCTCCCTGTCTCCGGGTAAA
661  -----+-----+----- 684
      TCGGAGAGGGACAGAGGCCCATTT
a      S  L  S  L  S  P  G  K

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FIGS. 4A and 4B

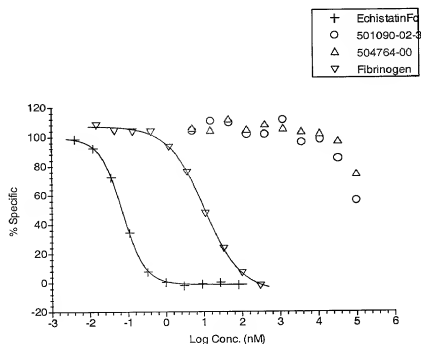
Inhibition of hu Vitronectin-Ru Binding to $\alpha v \beta 3$ 

Conc.		IC50 (pM)	Hill Slope	r ²	K _i
AMG	504823-05	26.73786	-1.14	1.000	21.10884
Conc.		IC50 (pM)	Hill Slope	r ²	K _i
AMG	EchistatinFc	0.12722	-1.10	0.999	0.10044
Conc.		IC50 (pM)	Hill Slope	r ²	K _i
AMG	504849-02	>10000			>10000
Conc.		IC50 (pM)	Hill Slope	r ²	K _i
AMG	501090-02-3	22.33247	-1.04	0.997	17.63090

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FIGS. 5A and 5B

Inhibition of hu Fibrinogen-Ru Binding To



nM

Conc.	IC50 (pM)	r2	Ki
AMG EchistatinFc	0.07187	1.000	0.03594

Conc.	IC50 (pM)	r2	Ki
AMG 501090-02-3	>100000		>100000

Conc.	IC50 (pM)	r2	Ki
AMG 504764-00	>100000		>100000

Conc.	IC50 (pM)	r2	Ki
AMG Fibrinogen	10.51409	0.999	5.25705